

# Protein: SEQUENCE COMPARISON w/ WO/0018915

ID AAY84609 standard; protein; 230 AA.  
 DT 25-JUL-2000 (first entry)  
 XX  
 DE A human membrane associated organizational protein (HJNCT).  
 XX  
 KW Human; membrane associated organizational protein; HJNCT;  
 KW cell proliferative disorder; cancer; autoimmune disorder;  
 KW inflammatory disorder; neurological disorder; developmental disorder;  
 KW vesicle trafficking; reproductive disorder; gastrointestinal disorder;  
 KW renal disorder; atherosclerosis; leukaemia; rheumatoid arthritis;  
 KW Alzheimer's disease; anxiety; diabetes; ovulatory defect; renal failure;  
 KW irritable bowel syndrome; allergy.

OS Homo sapiens.

FH	Key	Location/Qualifiers
FT	Modified-site	29
FT		/note= "potential phosphorylation site"
FT	Modified-site	62
FT		/note= "potential phosphorylation site"
FT	Domain	117..138
FT		/note= "transmembrane domain"
FT	Modified-site	155
FT		/note= "potential phosphorylation site"
FT	Domain	164..182
FT		/note= "transmembrane domain"
FT	Modified-site	187
FT		/note= "potential phosphorylation site"
FT	Modified-site	190
FT		/note= "potential glycosylation site"
FT	Modified-site	208
FT		/note= "potential phosphorylation site"
FT	Modified-site	224
FT		/note= "potential phosphorylation site"

PN WO200018915-A2.

PD 06-APR-2000.

PF 23-SEP-1999; 99WO-US022082.

PR 25-SEP-1998; 98US-0155215P.

PR 13-OCT-1998; 98US-0155251P.

PR 04-MAY-1999; 99US-0172228P.

PA (INCY-) INCYTE PHARM INC.

PI Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR, Lu AD, Tang YT;

DR WPI; 2000-293154/25.

DR N-PSDB; AAA12585.

PT Human membrane associated organizational protein and nucleic acid  
 PT sequences useful in the diagnosis, treatment and prevention of cell  
 PT proliferative associated disorders e.g. cancer, rheumatoid arthritis and  
 PT Alzheimer's disease.

XX

PS Claim 1; Page 76-77; 84pp; English.

XX

CC The present sequence represents a membrane associated organizational  
 CC protein (HJNCT). HJNCT is used for the diagnosis, treatment and  
 CC prevention of cell proliferative disorders including cancer and  
 CC autoimmune/inflammatory, neurological, developmental, vesicle  
 CC trafficking, reproductive, gastrointestinal and renal disorders. These  
 CC disorders may include atherosclerosis, leukaemia, allergies, rheumatoid  
 CC arthritis, Alzheimer's disease, anxiety, diabetes, ovulatory defects,  
 CC renal failure and irritable bowel syndrome. A vector expressing HJNCT,  
 CC and an agonist of HJNCT can be used to treat or prevent a disorder  
 CC associated with decreased expression or activity of HJNCT. An antagonist  
 CC of HJNCT or a vector expressing the complement of a polynucleotide  
 CC encoding HJNCT can be used to treat or prevent a disorder associated with  
 CC increased expression or activity of HJNCT. Antibodies which bind HJNCT  
 CC can be used for diagnosis of disorders associated with HJNCT expression  
 CC or to monitor patients being treated with HJNCT, agonists, antagonists or  
 CC inhibitors of HJNCT. Assays are preferably carried out on body fluids  
 CC from a patient using radioimmunoassay, enzyme linked immunosorbent assays  
 CC or fluorescent activated cell sorting assays. Polynucleotides encoding  
 CC HJNCT are also used in hybridisation assays to determine absence,  
 CC presence or excess expression of HJNCT and to monitor regulation of HJNCT  
 CC levels during disease therapy

XX

SQ Sequence 230 AA;

Query Match 100.0%; Score 1174; DB 3; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-117;  
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MASLGLQLVG	YILG	LLG	LLG	TLV	AM	LLP	SW	KTSS	YVG	AS	IV	TA	VG	FS	KGL	WME	CATH	STG	60		
Db	1	MASLGLQLVG	YILG	LLG	LLG	TLV	AM	LLP	SW	KTSS	YVG	AS	IV	TA	VG	FS	KGL	WME	CATH	STG	60		
Qy	61	ITQCDIYST	LLGL	PADI	QAAQ	AM	MTSS	AI	SSL	AC	II	SV	VG	MR	CT	VF	CQ	ES	RA	KDR	VAV	120	
Db	61	ITQCDIYST	LLGL	PADI	QAAQ	AM	MTSS	AI	SSL	AC	II	SV	VG	MR	CT	VF	CQ	ES	RA	KDR	VAV	120	
Qy	121	GGVFFILG	GLLG	FIPV	AWN	LHG	ILR	DFY	SPL	VP	DS	MK	FE	IG	EAL	YLG	II	SSL	FS	LI	AG	II	180
Db	121	GGVFFILG	GLLG	FIPV	AWN	LHG	ILR	DFY	SPL	VP	DS	MK	FE	IG	EAL	YLG	II	SSL	FS	LI	AG	II	180
Qy	181	LCFSCSSQ	RNRS	NY	YDAY	QAQ	PL	AT	RSS	PR	PG	QPP	KV	KSE	FNS	YS	LT	GY	V	230			
Db	181	LCFSCSSQ	RNRS	NY	YDAY	QAQ	PL	AT	RSS	PR	PG	QPP	KV	KSE	FNS	YS	LT	GY	V	230			

# Nucleic Acid: Sequence Comparison w/ w0018915

\*\*\*\*\*  
AF177340 1839 GGACAGGAAGGCAGCCTGGGACATTTAAAAAAA

→ >10 P\_AAA12585 cDNA encoding a membrane associated organizational protein (HJNCT). (2742 bp) [1 seg]

Score = 1472 (2918 bits), Expect = 0.0

Identities = 1472/1472 (100%), at 4,1-1475,1472, Strand +/+

```

ss.DNA64886  4 AGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGA
                *****
P_AAA12585    1 AGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGA

ss.DNA64886  64 GCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCAT
                *****
P_AAA12585   61 GCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCAT

ss.DNA64886  124 GGCCTCTCTTGGCCTCCAACCTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCAC
                *****
P_AAA12585   121 GGCCTCTCTTGGCCTCCAACCTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCAC

ss.DNA64886  184 ACTGGTTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGT
                *****
P_AAA12585   181 ACTGGTTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGT

ss.DNA64886  244 GACAGCAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCAT
                *****
P_AAA12585   241 GACAGCAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCAT

ss.DNA64886  304 CACCCAGTGTGACATCTATAGCACCTTCTGGGCCTGCCCGCTGACATCCAGGCTGCCCA
                *****
P_AAA12585   301 CACCCAGTGTGACATCTATAGCACCTTCTGGGCCTGCCCGCTGACATCCAGGCTGCCCA

ss.DNA64886  364 GGCCATGATGGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGG
                *****
P_AAA12585   361 GGCCATGATGGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGG

ss.DNA64886  424 CATGAGATGCACAGTCTTCTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGG
                *****
P_AAA12585   421 CATGAGATGCACAGTCTTCTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGG

ss.DNA64886  484 TGGAGTCTTTTTCATCCTTGGAGGCCTCCTGGGATTCATTCCTGTTGCCTGGAATCTTCA
                *****
P_AAA12585   481 TGGAGTCTTTTTCATCCTTGGAGGCCTCCTGGGATTCATTCCTGTTGCCTGGAATCTTCA

ss.DNA64886  544 TGGGATCCTACGGGACTTCTACTCACCCTGGTGCCTGACAGCATGAAATTTGAGATTGG
                *****
P_AAA12585   541 TGGGATCCTACGGGACTTCTACTCACCCTGGTGCCTGACAGCATGAAATTTGAGATTGG

ss.DNA64886  604 AGAGGCTCTTTACTTGGGCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCT
                *****
P_AAA12585   601 AGAGGCTCTTTACTTGGGCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCT

ss.DNA64886  664 CTGCTTTTCCTGCTCATCCCAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCA
                *****
P_AAA12585   661 CTGCTTTTCCTGCTCATCCCAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCA

ss.DNA64886  724 ACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTT

```

```

*****
P_AAA12585 721 ACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTT
ss.DNA64886 784 CAATTCCTACAGCCTGACAGGGTATGTGTGAAGAACCAGGGGCCAGAGCTGGGGGGTGGC
*****
P_AAA12585 781 CAATTCCTACAGCCTGACAGGGTATGTGTGAAGAACCAGGGGCCAGAGCTGGGGGGTGGC
ss.DNA64886 844 TGGGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACCACT
*****
P_AAA12585 841 TGGGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACCACT
ss.DNA64886 904 GGATCGTGTGAGAAGGTGCTGCTGAGGATAGACTGACTTTGGCCATTGGATTGAGCAAAG
*****
P_AAA12585 901 GGATCGTGTGAGAAGGTGCTGCTGAGGATAGACTGACTTTGGCCATTGGATTGAGCAAAG
ss.DNA64886 964 GCAGAAATGGGGGCTAGTGTAACAGCATGCAGGTTGAATTGCCAAGGATGCTCGCCATGC
*****
P_AAA12585 961 GCAGAAATGGGGGCTAGTGTAACAGCATGCAGGTTGAATTGCCAAGGATGCTCGCCATGC
ss.DNA64886 1024 CAGCCTTTCTGTTTTCTCACCTTGCTGCTCCCCTGCCCTAAGTCCCCAACCTCAACTT
*****
P_AAA12585 1021 CAGCCTTTCTGTTTTCTCACCTTGCTGCTCCCCTGCCCTAAGTCCCCAACCTCAACTT
ss.DNA64886 1084 GAAACCCCATTCCTTAAGCCAGGACTCAGAGGATCCCTTTGCCCTCTGGTTTACCTGGG
*****
P_AAA12585 1081 GAAACCCCATTCCTTAAGCCAGGACTCAGAGGATCCCTTTGCCCTCTGGTTTACCTGGG
ss.DNA64886 1144 ACTCCATCCCCAAACCCACTAATCACATCCCCTGACTGACCCTCTGTGATCAAAGACCC
*****
P_AAA12585 1141 ACTCCATCCCCAAACCCACTAATCACATCCCCTGACTGACCCTCTGTGATCAAAGACCC
ss.DNA64886 1204 TCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGGGGATGGGAAGGAGAAGCAGTGGC
*****
P_AAA12585 1201 TCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGGGGATGGGAAGGAGAAGCAGTGGC
ss.DNA64886 1264 TTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCC
*****
P_AAA12585 1261 TTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCC
ss.DNA64886 1324 TGGAACCTCCATCCCCTCTTGTTATGACTCCACAGTGTCCAGACTAATTTGTGCATGAA
*****
P_AAA12585 1321 TGGAACCTCCATCCCCTCTTGTTATGACTCCACAGTGTCCAGACTAATTTGTGCATGAA
ss.DNA64886 1384 CTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATGCAGGATGGGAGGA
*****
P_AAA12585 1381 CTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATGCAGGATGGGAGGA
ss.DNA64886 1444 CAGGAAGGCAGCCTGGGACATTTAAAAAATA
*****
P_AAA12585 1441 CAGGAAGGCAGCCTGGGACATTTAAAAAATA

```

>11 P\_AAF93769 Human cDNA encoding a membrane or secretory protein clone  
PSEC0059. (2863 bp) [1 seg]

Score = 1464 (2902 bits), Expect = 0.0

Identities = 1470/1472 (99%), at 1,110-1472,1581, Strand +/+

```

ss.DNA64886 1 GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCA

```

```
Query Match      100.0%;  Score 1174;  DB 2;  Length 230;
Best Local Similarity 100.0%;  Pred. No. 7.3e-117;
Matches 230;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
```

[illegible]

Db 181 LCFSCSSQRNRSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV 230



# Nucleic Acid: SEQUENCE COMPARISON w/w0/9925825

```

ss.DNA64886 887 TGAGGGACACTACCACTGGATCGTGTGAGAGGTGCTGCTGAGGATAGACTGACTTTGGC
*****
AX286822 842 TGAGGGACACTACCACTGGATCGTGTGAGAGGTGCTGCTGAGGATAGACTGACTTTGGC

ss.DNA64886 947 CATTGGA TTGAGCAAGGGGAGGAT GGGGGCTAGTGTAACAGCATGCAGGTGAATTG
*****
AX286822 902 CATTGGATTGAGCAAAGGCAGAAATGCCCCGCTAGGTATACAGCATGCGGTTGAATTG

ss.DNA64886 1005 CCAAGGATGCTCGCCATGCCAGCCCTTCTGTTTTCTCACCTTGCTGCTCCCCTGCCCTA
*****
AX286822 962 CCAAGGATGCTCGCCATGCCAGCCCTTCTGTTTTCTCACCTTGCTGCTCCCCTGCCCTA

ss.DNA64886 1065 AGTCCCAACCCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGGATCCCTTT
*****
AX286822 1022 AGTCCCAACCCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGGATCCCTTT

ss.DNA64886 1125 GCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCACTGACTGAC
*****
AX286822 1082 GCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCACTGACTGAC

ss.DNA64886 1185 CCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGGGGAT
*****
AX286822 1142 CCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGGGGAT

ss.DNA64886 1245 GCGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCTC
*****
AX286822 1202 GCGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCTC

ss.DNA64886 1305 CAAAGAACTGATTGGCCCTGGAACCTCCATCCCCTCTTGTATGACTCCACAGTGTCC
*****
AX286822 1262 CAAAGAACTGATTGGCCCTGGAACCTCCATCCCCTCTTGTATGACTCCACAGTGTCC

ss.DNA64886 1365 AGACTAATTGTGTCATGAAGTGAATAAAASCATCCTACGGTATCCAGGGAAGAGAAAGC
*****
AX286822 1322 AGACTAATTGTGTCATGAAGTGAATAAAACCATCCTACGGTATCCAGGGAAGAGAAAGC

ss.DNA64886 1425 AGGATGCAAGATGGGAGGACAGGAAGGAGCCTGGGACATTAAAAAATA
*****
AX286822 1382 AGGATGCAAGATGGGAGGACAGGAAGGAGCCTGGGACATTAAAAAATA

```

>18 P\_AAX97865 Human secreted protein encoding cDNA #53. cDNA, PAT 23-SEP-1999 (1400 bp) [1 seg]

Score = 1381 (2738 bits), Expect = 0.0

Identities = 1387/1389 (99%), at 87,1-1475,1389, Strand +/-

```

ss.DNA64886 87 CAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATGGCCTCTCTTGGCCTCCAAGT
*****
P_AAX97865 1 CAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATGGCCTCTCTTGGCCTCCAAGT

ss.DNA64886 147 TGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGTTGCCATGCTGCTCCCCA
*****
P_AAX97865 61 TGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGTTGCCATGCTGCTCCCCA

ss.DNA64886 207 GCTGGAAAACAAGTTCTTATGTGCGGTGCCAGCATTGTGACAGCAGTTGGCTTCTCCAAG
*****
P_AAX97865 121 GCTGGAAAACAAGTTCTTATGTGCGGTGCCAGCATTGTGACAGCAGTTGGCTTCTCCAAG

```

ss.DNA64886 267 GCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGACATCTATAGCA  
\*\*\*\*\*  
P\_AAX97865 181 GCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGACATCTATAGCA

ss.DNA64886 327 CCCTTCTGGGCCTGCCCCTGACATCCAGGCTGCCCAGGCCATGATGGTGACATCCAGTG  
\*\*\*\*\*  
P\_AAX97865 241 CCCTTCTGGGCCTGCCCCTGACATCCAGGCTGCCCAGGCCATGATGGTGACATCCAGTG

ss.DNA64886 387 CAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTTCTGCC  
\*\*\*\*\*  
P\_AAX97865 301 CAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTTCTGCC

ss.DNA64886 447 AGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTCATCCTTGAG  
\*\*\*\*\*  
P\_AAX97865 361 AGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTCATCCTTGAG

ss.DNA64886 507 GCCTCCTGGGATTCATTCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGACTTCTACT  
\*\*\*\*\*  
P\_AAX97865 421 GCCTCCTGGGATTCATTCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGACTTCTACT

ss.DNA64886 567 CACCACTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGGGCATT  
\*\*\*\*\*  
P\_AAX97865 481 CACCACTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGGGCATT

ss.DNA64886 627 TTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCCTGCTCATCCCAGA  
\*\*\*\*\*  
P\_AAX97865 541 TTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCCTGCTCATCCCAGA

ss.DNA64886 687 GAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTCTC  
\*\*\*\*\*  
P\_AAX97865 601 GAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTCTC

ss.DNA64886 747 CAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGT  
\*\*\*\*\*  
P\_AAX97865 661 CAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGT

ss.DNA64886 807 ATGTGTGAAGAACCAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGAC  
\*\*\*\*\*  
P\_AAX97865 721 ATGTGTGAAGAACCAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGAC

ss.DNA64886 867 AGCACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCT  
\*\*\*\*\*  
P\_AAX97865 781 AGCACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCT

ss.DNA64886 927 GAGGATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAAC  
\*\*\*\*\*  
P\_AAX97865 841 GAGGGTAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAAC

ss.DNA64886 987 AGCATGCAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCT  
\*\*\*\*\*  
P\_AAX97865 901 AGCATGCAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCT

ss.DNA64886 1047 TGCTGCTCCCCTGCCCTAAGTCCCCAACCCCTCAACTTGAAACCCCATTCCTTAAGCCAG  
\*\*\*\*\*  
P\_AAX97865 961 TGCTGCTCCCCTGCCCTAAGTCCCCAACCCCTCAACTTGAAACCCCATTCCTTAAGCCAG



ss.DNA64886 1107 GACTCAGAGGATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAAT  
\*\*\*\*\*  
P\_AAX97865 1021 GACTCAGAGGATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAAT

ss.DNA64886 1167 CACATCCCCTGACTGACCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCT  
\*\*\*\*\*  
P\_AAX97865 1081 CACATCCCCTGACTGACCCTCTGTGATCAAAGACCCTCCCTCTGGCTGAGGTTGGCTCT  
4

ss.DNA64886 1227 TAGCTCATTGCTGGGGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCT  
\*\*\*\*\*  
P\_AAX97865 1141 TAGCTCATTGCTGGGGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCT

ss.DNA64886 1287 ACTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCCTCTTGT  
\*\*\*\*\*  
P\_AAX97865 1201 ACTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCCTCTTGT

ss.DNA64886 1347 TATGACTCCACAGTGTCCAGACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGT  
\*\*\*\*\*  
P\_AAX97865 1261 TATGACTCCACAGTGTCCAGACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGT

ss.DNA64886 1407 ATCCAGGGAACAGAAAGCAGGATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTT  
\*\*\*\*\*  
P\_AAX97865 1321 ATCCAGGGAACAGAAAGCAGGATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTT

ss.DNA64886 1467 AAAAAAATA  
\*\*\*\*\*  
P\_AAX97865 1381 AAAAAAATA

```
Query Match      93.4%;   Score 1096;   DB 1;   Length 230;
Best Local Similarity 91.3%;   Pred. No. 1.4e-85;
Matches 210;   Conservative 11;   Mismatches 9;   Indels 0;   Gaps 0;
```

```

Qy      1 MASLGLQLVGYYILGLLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTG 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 MASLGVQLVGYYILGLLGLLGTSIAMLLPNWRTSSYVGASIVTAVGFSKGLWMECATHSTG 60

Qy      61 ITQCDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVA 120
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

```

Db          61 ITQCDIYSTLLGLPADIQAAQAMMVTSSAMSSLACIISVVGMRCTVFCQDSRAKDRVAVV 120
Qy          121 GGVFFILGGLLGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGII 180
          |||||:|||||
Db          121 GGVFFILGGILGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIIISALFSLVAGVI 180
Qy          181 LCFSCSSQRNRSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNSSYSLTGYV 230
          ||||| | ||:|||||
Db          181 LCFSCSPQGNRTNYYDGYQAQPLATRSSPRSAQQPKAKSEFNSSYSLTGYV 230

```